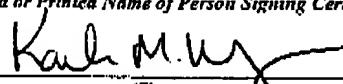


CERTIFICATE OF TRANSMISSION BY FACSIMILE (37 CFR 1.8) Applicant(s): Dario Alessi et al.			Docket No. 002.00170
Application No. 09/937,009	Filing Date March 17, 2000	Examiner M. Monshipouri	Group Art Unit 1653
Invention: ENZYME			
<p>I hereby certify that this <u>Copy of Sequence Listing as submitted on June 26, 2002 (26 pgs)</u> <small>(Identify type of correspondence)</small> is being facsimile transmitted to the United States Patent and Trademark Office (Fax. No. <u>571 273-0932</u>) on <u>Feb. 7, 2006</u> <small>(Date)</small></p> <p style="text-align: right;">Karla M. Weyand <small>(Typed or Printed Name of Person Signing Certificate)</small>  <small>(Signature)</small></p>			
<p>Note: Each paper must have its own certificate of mailing.</p> <p>BEST AVAILABLE COPY</p>			

SEQUENCE LISTING

<110> Alessi, Dario
Balendran, Anudharan
Deak, Maria
Currie, Richard
Downes, Peter
Casamayor, Antonio

<120> Enzyme

<130> 002.00170

<140> US 09/937,009
<141> 2000-03-17

<150> PCT/GB00/01004
<151> 2000-03-17

<150> GB 9906245.7
<151> 1999-03-19

<160> 34

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

<220>
<223> region B of PRK2

<400> 1
Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Phe Arg Asp
1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys
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<211> 24
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic peptide sequence that interacts with human PRK2 region B

<400> 2
Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Ala Arg Asp
1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys
20

<210> 3

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic peptide sequence that interacts with human PRK2 region B

<400> 3
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1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys
20

<210> 4

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<223> region A of PRK2

<400> 4

Glu Asp Val Lys Lys His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala
1 5 10 15

Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly
20 25 30

Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro
35 40 45

Ile Leu Thr Pro Pro
50

<210> 5
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKC zeta

<400> 5
Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Gly Phe
1 5 10 15

Glu Tyr Ile Asn Pro Leu Leu
20

<210> 6
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<223> portion of region B of PRK2

<400> 6
Phe Arg Asp Phe Asp Tyr
1 5

<210> 7
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKC zeta

<400> 7
Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Gly Phe
1 5 10 15

Glu Tyr Ile Asn Pro Leu Leu
20

<210> 8
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKB alpha

<400> 8
Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser
1 5 10

<210> 9
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> region of PRK1

<400> 9
Thr Phe Cys Gly Thr Pro Glu Phe Leu
1 5

<210> 10
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKC zeta

<400> 10
Phe Glu Gly Phe Glu Tyr
1 5

<210> 11
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<223> region of PDK1

<400> 11
Arg Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
1 5 10

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pcr primer

<400> 12
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28

<210> 13
<211> 7
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human PKB alpha
substrate peptide

<400> 13
Arg Pro Arg Thr Ala Ala Phe
1 5

<210> 14
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<223> region of PRK2

<400> 14
Glu Asp Val Lys Lys His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala
1 5 10 15

Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly
20 25 30

Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro
35 40 45

Ile Leu Thr Pro Pro Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln
50 55 60

Glu Met Phe Arg Asp Phe Asp Tyr Ile Ala Asp Trp Cys
65 70 75

<210> 15
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<223> region of PRK1

<400> 15
Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr Leu Gly Trp Glu Ala
1 5 10 15

Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser Gly
20 25 30

Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala Pro
35 40 45

Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu Gln
50 55 60

Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys
65 70 75

<210> 16
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<223> region of PKB alpha

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Lys Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His
1 5 10 15

Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser
20 25 30

Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile
35 40 45

Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser
50 55 60

Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Thr Ala
65 70 75 80

<210> 17

<211> 75

<212> PRT

<213> Homo sapiens

<220>

<223> region of P70S6k

<400> 17

Gly Glu Val Gln Ala His Pro Phe Phe Arg His Ile Asn Trp Glu Glu
1 5 10 15

Leu Leu Ala Arg Lys Val Glu Pro Pro Phe Lys Pro Leu Leu Gln Ser
20 25 30

Glu Glu Asp Val Ser Gln Phe Asp Ser Lys Phe Thr Arg Gln Thr Pro
35 40 45

Val Asp Ser Pro Asp Asp Ser Thr Leu Ser Glu Ser Ala Asn Gln Val
50 55 60

Phe Leu Gly Phe Thr Tyr Val Ala Pro Ser Val

65 70 75

<210> 18

<211> 82

<212> PRT

<213> Homo sapiens

<220>

<223> region of SGK

<400> 18

Met Glu Ile Lys Ser His Val Phe Phe Ser Leu Ile Asn Trp Asp Asp

10 15

Leu Ile Asn Lys Lys Ile Thr Pro Pro Phe Asn Pro Asn Val Ser Gly
20 25 30

Pro Asn Glu Leu Arg His Phe Asp Pro Glu Phe Thr Glu Glu Pro Val
35 40 45

Pro Asn Ser Ile Gly Lys Ser Pro Asp Ser Val Leu Val Thr Ala Ser
50 55 60

Val Lys Glu Ala Ala Glu Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro
65 70 75 80

Thr Asp

<210> 19

<211> 76

<212> PRT

<213> Homo sapiens

52202

<223> region of PKC zeta

<400> 19

Ser Asp Ile Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu
 1 5 10 15

Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp
20 25 30

Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val
35 40 45

Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser
50 55 60

Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro Leu Leu
65 70 75

<210> 20
<211> 75
<212> PRT
<213> *Homo sapiens*

<220>

<223> region of PKC alpha

<400> 20

Arg Asp Val Arg Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys
1 5 10 15

Leu Glu Asn Arg Glu Ile Glu Pro Pro Phe Lys Pro Lys Val Cys Gly
20 25 30

Lys Gly Ala Glu Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val
35 40 45

Leu Thr Pro Pro Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp
50 55 60

Phe Glu Gly Phe Ser Tyr Val Asn Pro Gln Phe
65 70 75

<210> 21

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<223> region of PKA beta

<400> 21

Ser Asp Ile Lys Thr His Lys Trp Phe Ala Thr Thr Asp Trp Ile Ala
1 5 10 15

Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Gly Arg
20 25 30

Ser Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Asp Ile Arg
35 40 45

Val Ser Ile Thr Glu Cys Ala Lys Glu Lys Phe Gly Glu Phe
50 55 60

<210> 22

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residues 2 and 3 are variable amino acids

<400> 22

Phe Xaa Xaa Phe Ser Phe

1

5

<210> 23

<211> 8

<212> PRT

<213> Homo sapiens

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<223> PKB consensus sequence

<220>

<223> residue 6 is a variable amino acid

<400> 23

Thr Phe Cys Gly Thr Xaa Glu Leu

1

5

<210> 24

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> PKB consensus sequence

<220>

<223> residues 2 and 3 are variable amino acids

<220>

<223> residue 5 is serine or threonine

<220>

<223> residue 6 is phenylalanine or tyrosine

<400> 24

Phe Xaa Xaa Phe Xaa Xaa

1

5

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:synthetic sequence that interacts with PKB

<220>
<223> residues 2 and 3 are variable amino acids

<220>
<223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>
<223> residue 5 is a negatively charged amino acid

<400> 25
Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 26
<211> 6
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<220>
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<220>
<223> residues 2 and 3 are variable amino acids

<220>
<223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>
<223> residue 5 is aspartic acid or glutamic acid

<400> 26
Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 27
<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic sequence that interacts with PKB

<220>

<223> residues 2 and 3 are variable amino acids

<220>

<223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>

<223> residue 5 is phospho serine or phospho threonine

<400> 27

Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 28

<211> 8

<212> PRT

<213> Homo sapiens

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<223> PKB consensus sequence

<220>

<223> residue 1 is threonine or serine

<220>

<223> residue 6 is a variable amino acid

<400> 28

Xaa Phe Cys Gly Thr Xaa Glu Leu

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<210> 29

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> C terminal region of PKC zeta

<400> 29
Phe Glu Gly Phe Glu Tyr
1 5

<210> 30
<211> 6
<212> PRT
<213> Homo sapiens

<220>
<223> PKB consensus sequence

<220>
<223> residues 1, 4 and 6 are phenylalanine or tyrosine

<220>
<223> residues 2 and 3 are variable amino acids

<220>
<223> residue 5 is serine or threonine

<400> 30
Xaa Xaa Xaa Xaa Xaa Xaa
1 5

<210> 31
<211> 556
<212> PRT
<213> Homo sapiens

<220>
<223> PDK1 sequence

<400> 31
Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser
1 5 10 15

Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
20 25 30

Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
35 40 45

Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
50 55 60

Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
 65 70 75 80
 Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
 85 90 95
 Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile
 100 105 110
 Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
 115 120 125
 Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
 130 135 140
 Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
 145 150 155 160
 Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser
 165 170 175
 Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
 180 185 190
 Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
 195 200 205
 Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
 210 215 220
 Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
 225 230 235 240
 Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
 245 250 255
 Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
 260 265 270
 Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
 275 280 285
 Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys
 290 295 300
 Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp
 305 310 315 320

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu
325 330 335

Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln
340 345 350

Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp
355 360 365

Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly
370 375 380

Cys Met Gln Val Ser Ser Ser Ser His Ser Leu Ser Ala Ser
385 390 395 400

Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile
405 410 415

His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu
420 425 430

Asp Glu Lys Arg Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp
435 440 445

His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp
450 455 460

Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu
465 470 475 480

Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly
485 490 495

Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys
500 505 510

Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro
515 520 525

Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg
530 535 540

Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
545 550 555

<210> 32
<211> 984

<212> PRT

<213> Homo sapiens

<220>

<223> PRK2 sequence

<400> 32

Met Ala Ser Asn Pro Glu Arg Gly Glu Ile Leu Leu Thr Glu Leu Gln
1 5 10 15

Gly Asp Ser Arg Ser Leu Pro Phe Ser Glu Asn Val Ser Ala Val Gln
20 25 30

Lys Leu Asp Phe Ser Asp Thr Met Val Gln Gln Lys Leu Asp Asp Ile
35 40 45

Lys Asp Arg Ile Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu
50 55 60

Gly Ala Glu Asn Leu Arg Lys Val Thr Thr Asp Lys Lys Ser Leu Ala
65 70 75 80

Tyr Val Asp Asn Ile Leu Lys Lys Ser Asn Lys Lys Leu Glu Glu Leu
85 90 95

His His Lys Leu Gln Glu Leu Asn Ala His Ile Val Val Ser Asp Pro
100 105 110

Glu Asp Ile Thr Asp Cys Pro Arg Thr Pro Asp Thr Pro Asn Asn Asp
115 120 125

Pro Arg Cys Ser Thr Ser Asn Asn Arg Leu Lys Ala Leu Gln Lys Gln
130 135 140

Leu Asp Ile Glu Leu Lys Val Lys Gln Gly Ala Glu Asn Met Ile Gln
145 150 155 160

Met Tyr Ser Asn Gly Ser Ser Lys Asp Arg Lys Leu His Gly Thr Ala
165 170 175

Gln Gln Leu Leu Gln Asp Ser Lys Thr Lys Ile Glu Val Ile Arg Met
180 185 190

Gln Ile Leu Gln Ala Val Gln Thr Asn Glu Leu Ala Phe Asp Asn Ala
195 200 205

Lys Pro Val Ile Ser Pro Leu Glu Leu Arg Met Glu Glu Leu Arg His
210 215 220

His Phe Arg Ile Glu Phe Ala Val Ala Glu Gly Ala Lys Asn Val Met
225 230 235 240

Lys Leu Leu Gly Ser Gly Lys Val Thr Asp Arg Lys Ala Leu Ser Glu
245 250 255

Ala Gln Ala Arg Phe Asn Glu Ser Ser Gln Lys Leu Asp Leu Leu Lys
260 265 270

Tyr Ser Leu Glu Gln Arg Leu Asn Glu Val Pro Lys Asn His Pro Lys
275 280 285

Ser Arg Ile Ile Ile Glu Glu Leu Ser Leu Val Ala Ala Ser Pro Thr
290 295 300

Leu Ser Pro Arg Gln Ser Met Ile Ser Thr Gln Asn Gln Tyr Ser Thr
305 310 315 320

Leu Ser Lys Pro Ala Ala Leu Thr Gly Thr Leu Glu Val Arg Leu Met
325 330 335

Gly Cys Gln Asp Ile Leu Glu Asn Val Pro Gly Arg Ser Lys Ala Thr
340 345 350

Ser Val Ala Leu Pro Gly Trp Ser Pro Ser Glu Thr Arg Ser Ser Phe
355 360 365

Met Ser Arg Thr Ser Lys Ser Lys Ser Gly Ser Ser Arg Asn Leu Leu
370 375 380

Lys Thr Asp Asp Leu Ser Asn Asp Val Cys Ala Val Leu Lys Leu Asp
385 390 395 400

Asn Thr Val Val Gly Gln Thr Ser Trp Lys Pro Ile Ser Asn Gln Ser
405 410 415

Trp Asp Gln Lys Phe Thr Leu Glu Leu Asp Arg Ser Arg Glu Leu Glu
420 425 430

Ile Ser Val Tyr Trp Arg Asp Trp Arg Ser Leu Cys Ala Val Lys Phe
435 440 445

Leu Arg Leu Glu Asp Phe Leu Asp Asn Gln Arg His Gly Met Cys Leu
450 455 460

Tyr Leu Glu Pro Gln Gly Thr Leu Phe Ala Glu Val Thr Phe Phe Asn
465 470 475 480

Pro Val Ile Glu Arg Arg Pro Lys Leu Gln Arg Gln Lys Lys Ile Phe
485 490 495

Ser Lys Gln Gln Gly Lys Thr Phe Leu Arg Ala Pro Gln Met Asn Ile
500 505 510

Asn Ile Ala Thr Trp Gly Arg Leu Val Arg Arg Ala Ile Pro Thr Val
515 520 525

Asn His Ser Gly Thr Phe Ser Pro Gln Ala Pro Val Pro Thr Thr Val
530 535 540

Pro Val Val Asp Val Arg Ile Pro Gln Leu Ala Pro Pro Ala Ser Asp
545 550 555 560

Ser Thr Val Thr Lys Leu Asp Phe Asp Leu Glu Pro Glu Pro Pro Pro
565 570 575

Ala Pro Pro Arg Ala Ser Ser Leu Gly Glu Ile Asp Glu Ser Ser Glu
580 585 590

Leu Arg Val Leu Asp Ile Pro Gly Gln Asp Ser Glu Thr Val Phe Asp
595 600 605

Ile Gln Asn Asp Arg Asn Ser Ile Leu Pro Lys Ser Gln Ser Glu Tyr
610 615 620

Lys Pro Asp Thr Pro Gln Ser Gly Leu Glu Tyr Ser Gly Ile Gln Glu
625 630 635 640

Leu Glu Asp Arg Arg Ser Gln Gln Arg Phe Gln Phe Asn Leu Gln Asp
645 650 655

Phe Arg Cys Cys Ala Val Leu Gly Arg Gly His Phe Gly Lys Val Leu
660 665 670

Leu Ala Glu Tyr Lys Asn Thr Asn Glu Met Phe Ala Ile Lys Ala Leu
675 680 685

Lys Lys Gly Asp Ile Val Ala Arg Asp Glu Val Asp Ser Leu Met Cys
690 695 700

Glu Lys Arg Ile Phe Glu Thr Val Asn Ser Val Arg His Pro Phe Leu
705 710 715 720

Val Asn Leu Phe Ala Cys Phe Gln Thr Lys Glu His Val Cys Phe Val
725 730 735

Met Glu Tyr Ala Ala Gly Gly Asp Leu Met Met His Ile His Thr Asp
740 745 750

Val Phe Ser Glu Pro Arg Ala Val Phe Tyr Ala Ala Cys Val Val Leu
755 760 765

Gly Leu Gln Tyr Leu His Glu His Lys Ile Val Tyr Arg Asp Leu Lys
770 775 780

Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly Phe Val Lys Ile Ala Asp
785 790 795 800

Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr Gly Asp Arg Thr Ser Thr
805 810 815

Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro Glu Val Leu Thr Glu Thr
820 825 830

Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly Leu Gly Val Leu Ile Tyr
835 840 845

Glu Met Leu Val Gly Glu Ser Pro Phe Pro Gly Asp Asp Glu Glu Glu
850 855 860

Val Phe Asp Ser Ile Val Asn Asp Glu Val Arg Tyr Pro Arg Phe Leu
865 870 875 880

Ser Thr Glu Ala Ile Ser Ile Met Arg Arg Leu Leu Arg Arg Asn Pro
885 890 895

Glu Arg Arg Leu Gly Ala Ser Glu Lys Asp Ala Glu Asp Val Lys Lys
900 905 910

His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala Leu Met Asp Lys Lys
915 920 925

Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly Arg Glu Asp Val Ser
930 935 940

Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro Ile Leu Thr Pro Pro
945 950 955 960

Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln Glu Met Phe Arg Asp
965 970 975

Phe Asp Tyr Ile Ala Asp Trp Cys
980

<210> 33
<211> 942
<212> PRT
<213> Homo sapiens

<220>
<223> PRK1 sequence

<400> 33

Met Ala Ser Asp Ala Val Gln Ser Glu Pro Arg Ser Trp Ser Leu Leu
1 5 10 15

Glu Gln Leu Gly Leu Ala Gly Ala Asp Leu Ala Ala Pro Gly Val Gln
20 25 30

Gln Gln Leu Glu Leu Glu Arg Glu Arg Leu Arg Arg Glu Ile Arg Lys
35 40 45

Glu Leu Lys Leu Lys Glu Gly Ala Glu Asn Leu Arg Arg Ala Thr Thr
50 55 60

Asp Leu Gly Arg Ser Leu Gly Pro Val Glu Leu Leu Leu Arg Gly Ser
65 70 75 80

Ser Arg Arg Leu Asp Leu Leu His Gln Gln Leu Gln Glu Leu His Ala
85 90 95

His Val Val Leu Pro Asp Pro Ala Ala Thr His Asp Gly Pro Gln Ser
100 105 110

Pro Gly Ala Gly Gly Pro Thr Cys Ser Ala Thr Asn Leu Ser Arg Val
115 120 125

Ala Gly Leu Glu Lys Gln Leu Ala Ile Glu Leu Lys Val Lys Gln Gly
130 135 140

Ala Glu Asn Met Ile Gln Thr Tyr Ser Asn Gly Ser Thr Lys Asp Arg
145 150 155 160

Lys Leu Leu Leu Thr Ala Gln Gln Met Leu Gln Asp Ser Lys Thr Lys
165 170 175

Ile Asp Ile Ile Arg Met Gln Leu Arg Arg Ala Leu Gln Ala Asp Gln
180 185 190

Leu Glu Asn Gln Ala Ala Pro Asp Asp Thr Gln Gly Ser Pro Asp Leu

195	200	205
Gly Ala Val Glu Leu Arg Ile Glu Glu Leu Arg His His Phe Arg Val		
210	215	220
Glu His Ala Val Ala Glu Gly Ala Lys Asn Val Leu Arg Leu Leu Ser		
225	230	235
Ala Ala Lys Ala Pro Asp Arg Lys Ala Val Ser Glu Ala Gln Glu Lys		
245	250	255
Leu Thr Glu Ser Asn Gln Lys Leu Gly Leu Leu Arg Glu Ala Leu Glu		
260	265	270
Arg Arg Leu Gly Glu Leu Pro Ala Asp His Pro Lys Gly Arg Leu Leu		
275	280	285
Arg Glu Glu Leu Ala Ala Ser Ser Ala Ala Phe Ser Thr Arg Leu		
290	295	300
Ala Gly Pro Phe Pro Ala Thr His Tyr Ser Thr Leu Cys Lys Pro Ala		
305	310	315
Pro Leu Thr Gly Thr Leu Glu Val Arg Val Val Gly Cys Arg Asp Leu		
325	330	335
Pro Glu Thr Ile Pro Trp Asn Pro Thr Pro Ser Met Gly Gly Pro Gly		
340	345	350
Thr Pro Asp Ser Arg Pro Pro Phe Leu Ser Arg Pro Ala Arg Gly Leu		
355	360	365
Tyr Ser Arg Ser Gly Ser Leu Ser Gly Arg Ser Ser Leu Lys Ala Glu		
370	375	380
Ala Glu Asn Thr Ser Glu Val Ser Thr Val Leu Lys Leu Asp Asn Thr		
385	390	395
Val Val Gly Gln Thr Ser Trp Lys Pro Cys Gly Pro Asn Ala Trp Asp		
405	410	415
Gln Ser Phe Thr Leu Glu Leu Arg Ala Arg Glu Leu Glu Leu Ala		
420	425	430
Val Phe Trp Arg Asp Gln Arg Gly Leu Cys Ala Leu Lys Phe Leu Lys		
435	440	445
Leu Glu Asp Phe Leu Asp Asn Glu Arg His Glu Val Gln Leu Asp Met		

450	455	460
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Ile Glu Arg Ile Pro Arg Leu Arg Arg Gln Lys Lys Ile Phe Ser Lys		
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Gln Gln Gly Lys Ala Phe Gln Arg Ala Arg Gln Met Asn Ile Asp Val		
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Ala Thr Trp Val Arg Leu Leu Arg Arg Leu Ile Pro Asn Ala Thr Gly		
515	520	525
Thr Gly Thr Phe Ser Pro Gly Ala Ser Pro Gly Ser Glu Ala Arg Thr		
530	535	540
Thr Gly Asp Ile Ser Val Glu Lys Leu Asn Leu Gly Thr Asp Ser Asp		
545	550	555
Ser Ser Pro Gln Lys Ser Ser Arg Asp Pro Pro Ser Ser Pro Ser Ser		
565	570	575
Leu Ser Ser Pro Ile Gln Glu Ser Thr Ala Pro Glu Leu Pro Ser Glu		
580	585	590
Thr Gln Glu Thr Pro Gly Pro Ala Leu Cys Ser Pro Leu Arg Lys Ser		
595	600	605
Pro Leu Thr Leu Glu Asp Phe Lys Phe Leu Ala Val Leu Gly Arg Gly		
610	615	620
His Phe Gly Lys Val Leu Leu Ser Glu Phe Arg Pro Ser Gly Glu Leu		
625	630	635
Phe Ala Ile Lys Ala Leu Lys Lys Gly Asp Ile Val Ala Arg Asp Glu		
645	650	655
Val Glu Ser Leu Met Cys Glu Lys Arg Ile Leu Ala Ala Val Thr Ser		
660	665	670
Ala Gly His Pro Phe Leu Val Asn Leu Phe Gly Cys Phe Gln Thr Pro		
675	680	685
Glu His Val Cys Phe Val Met Glu Tyr Ser Ala Gly Gly Asp Leu Met		
690	695	700
Leu His Ile His Ser Asp Val Phe Ser Glu Pro Arg Ala Ile Phe Tyr		

705 710 715 720
Ser Ala Cys Val Val Leu Gly Leu Gln Phe Leu His Glu His Lys Ile
725 730 735

Val Tyr Arg Asp Leu Lys Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly
740 745 750

Tyr Val Lys Ile Ala Asp Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr
755 760 765

Gly Asp Arg Thr Ser Thr Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro
770 775 780

Glu Val Leu Thr Asp Thr Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly
785 790 795 800

Leu Gly Val Leu Leu Tyr Glu Met Leu Val Gly Glu Ser Pro Phe Pro
805 810 815

Gly Asp Asp Glu Glu Val Phe Asp Ser Ile Val Asn Asp Glu Val
820 825 830

Arg Tyr Pro Arg Phe Leu Ser Ala Glu Ala Ile Gly Ile Met Arg Arg
835 840 845

Leu Leu Arg Arg Asn Pro Glu Arg Arg Leu Gly Ser Ser Glu Arg Asp
850 855 860

Ala Glu Asp Val Lys Lys Gln Pro Phe Phe Arg Thr Leu Gly Trp Glu
865 870 875 880

Ala Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser
885 890 895

Gly Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala
900 905 910

Pro Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu
915 920 925

Gln Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys
930 935 940

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<212> PRT

<213> Homo sapiens

<220>

<223> PKC zeta sequence

<400> 34

Met Pro Ser Arg Thr Asp Pro Lys Met Glu Gly Ser Gly Gly Arg Val
1 5 10 15

Arg Leu Lys Ala His Tyr Gly Gly Asp Ile Phe Ile Thr Ser Val Asp
20 25 30

Ala Ala Thr Thr Phe Glu Glu Leu Cys Glu Glu Val Arg Asp Met Cys
35 40 45

Arg Leu His Gln Gln His Pro Leu Thr Leu Lys Trp Val Asp Ser Glu
50 55 60

Gly Asp Pro Cys Thr Val Ser Ser Gln Met Glu Leu Glu Glu Ala Phe
65 70 75 80

Arg Leu Ala Arg Gln Cys Arg Asp Glu Gly Leu Ile Ile His Val Phe
85 90 95

Pro Ser Thr Pro Glu Gln Pro Gly Leu Pro Cys Pro Gly Glu Asp Lys
100 105 110

Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu Tyr Arg Ala
115 120 125

Asn Gly His Leu Phe Gln Ala Lys Arg Phe Asn Arg Arg Ala Tyr Cys
130 135 140

Gly Gln Cys Ser Glu Arg Ile Trp Gly Leu Ala Arg Gln Gly Tyr Arg
145 150 155 160

Cys Ile Asn Cys Lys Leu Leu Val His Lys Arg Cys His Gly Leu Val
165 170 175

Pro Leu Thr Cys Arg Lys His Met Asp Ser Val Met Pro Ser Gln Glu
180 185 190

Pro Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu
195 200 205

Thr Asp Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Ser Ile
210 215 220

Lys Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly
225 230 235 240

Ile Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg
245 250 255

Val Ile Gly Arg Gly Thr Tyr Ala Lys Val Leu Leu Val Arg Leu Lys
260 265 270

Lys Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val
275 280 285

His Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe
290 295 300

Glu Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe
305 310 315 320

Gln Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly
325 330 335

Asp Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His
340 345 350

Ala Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His
355 360 365

Glu Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu
370 375 380

Asp Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu
385 390 395 400

Gly Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn
405 410 415

Tyr Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val
420 425 430

Asp Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg
435 440 445

Ser Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp
450 455 460

Tyr Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe
465 470 475 480

Leu Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp
485 490 495

Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile
500 505 510

Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys
515 520 525

Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly
530 535 540

Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr
545 550 555 560

Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu
565 570 575

Gly Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val
580 585 590

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